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## RAW SEQUENCE LISTING

DATE: 03/01/2002

PATENT APPLICATION: US/10/077,040

TIME: 12:43:17

Input Set : N:\Crf3\RULE60\10077040.raw

Output Set: N:\CRF3\03012002\J077040.raw

## SEQUENCE LISTING

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3 (1) GENERAL INFORMATION:
5     (i) APPLICANT: Lal, Preeti
6             Corley, Neil C.
7             Patterson, Chandra
9     (ii) TITLE OF INVENTION: HUMAN NEUROSECRETORY PROTEINS
11    (iii) NUMBER OF SEQUENCES: 6
13    (iv) CORRESPONDENCE ADDRESS:
14            (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
15            (B) STREET: 3174 Porter Dr.
16            (C) CITY: Palo Alto
17            (D) STATE: CA
18            (E) COUNTRY: USA
19            (F) ZIP: 94304
21    (v) COMPUTER READABLE FORM:
22            (A) MEDIUM TYPE: Diskette
23            (B) COMPUTER: IBM Compatible
24            (C) OPERATING SYSTEM: DOS
25            (D) SOFTWARE: FastSEQ for Windows Version 2.0
27    (vi) CURRENT APPLICATION DATA:
C--> 28            (A) APPLICATION NUMBER: US/10/077,040
C--> 29            (B) FILING DATE: 14-Feb-2002
30            (C) CLASSIFICATION:
32    (vii) PRIOR APPLICATION DATA:
33            (A) APPLICATION NUMBER: 09/062,601
34            (B) FILING DATE:
37    (viii) ATTORNEY/AGENT INFORMATION:
38            (A) NAME: Cerrone, Michael C.
39            (B) REGISTRATION NUMBER: 39,132
40            (C) REFERENCE/DOCKET NUMBER: PF-0510 US
42    (ix) TELECOMMUNICATION INFORMATION:
43            (A) TELEPHONE: 650-855-0555
44            (B) TELEFAX: 650-845-4166
45            (C) TELEX:
48 (2) INFORMATION FOR SEQ ID NO: 1:
50     (i) SEQUENCE CHARACTERISTICS:
51            (A) LENGTH: 468 amino acids
52            (B) TYPE: amino acid
53            (C) STRANDEDNESS: single
54            (D) TOPOLOGY: linear
56    (vii) IMMEDIATE SOURCE:
57            (A) LIBRARY: ISLTNOT01
58            (B) CLONE: 2379427

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60      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
62 Met Gly Phe Leu Gly Thr Gly Thr Trp Ile Leu Val Leu Val Leu Pro
63   1           5           10           15
64 Ile Gln Ala Phe Pro Lys Pro Gly Gly Ser Gln Asp Lys Ser Leu His
65           20           25           30
66 Asn Arg Glu Leu Ser Ala Glu Arg Pro Leu Asn Glu Gln Ile Ala Glu
67           35           40           45
68 Ala Glu Glu Asp Lys Ile Lys Lys Thr Tyr Pro Pro Glu Asn Lys Pro
69           50           55           60
70 Gly Gln Ser Asn Tyr Ser Phe Val Asp Asn Leu Asn Leu Leu Lys Ala
71           65           70           75           80
72 Ile Thr Glu Lys Glu Lys Ile Glu Lys Glu Arg Gln Ser Ile Arg Ser
73           85           90           95
74 Ser Pro Leu Asp Asn Lys Leu Asn Val Glu Asp Val Asp Ser Thr Lys
75           100          105          110
76 Asn Arg Lys Leu Ile Asp Asp Tyr Asp Ser Thr Lys Ser Gly Leu Asp
77           115          120          125
78 His Lys Phe Gln Asp Asp Pro Asp Gly Leu His Gln Leu Asp Gly Thr
79           130          135          140
80 Pro Leu Thr Ala Glu Asp Ile Val His Lys Ile Ala Ala Arg Ile Tyr
81           145          150          155          160
82 Glu Glu Asn Asp Arg Ala Val Phe Asp Lys Ile Val Ser Lys Leu Leu
83           165          170          175
84 Asn Leu Gly Leu Ile Thr Glu Ser Gln Ala His Thr Leu Glu Asp Glu
85           180          185          190
86 Val Ala Glu Val Leu Gln Lys Leu Ile Ser Lys Glu Ala Asn Asn Tyr
87           195          200          205
88 Glu Glu Asp Pro Asn Lys Pro Thr Ser Trp Thr Glu Asn Gln Ala Gly
89           210          215          220
90 Lys Ile Pro Glu Lys Val Thr Pro Met Ala Ala Ile Gln Asp Gly Leu
91           225          230          235          240
92 Ala Lys Gly Glu Asn Asp Glu Thr Val Ser Asn Thr Leu Thr Leu Thr
93           245          250          255
94 Asn Gly Leu Glu Arg Arg Thr Lys Thr Tyr Ser Glu Asp Asn Phe Glu
95           260          265          270
96 Glu Leu Gln Tyr Phe Pro Asn Phe Tyr Ala Leu Leu Lys Ser Ile Asp
97           275          280          285
98 Ser Glu Lys Glu Ala Lys Glu Lys Glu Thr Leu Ile Thr Ile Met Lys
99           290          295          300
100 Thr Leu Ile Asp Phe Val Lys Met Met Val Lys Tyr Gly Thr Ile Ser
101           305          310          315          320
102 Pro Glu Glu Gly Val Ser Tyr Leu Glu Asn Leu Asp Glu Met Ile Ala
103           325          330          335
104 Leu Gln Thr Lys Asn Lys Leu Glu Lys Asn Ala Thr Asp Asn Ile Ser
105           340          345          350
106 Lys Leu Phe Pro Ala Pro Ser Glu Lys Ser His Glu Glu Thr Asp Ser
107           355          360          365
108 Thr Lys Glu Glu Ala Ala Lys Met Glu Lys Glu Tyr Gly Ser Leu Lys
109           370          375          380

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110 Asp Ser Thr Lys Asp Asp Asn Ser Asn Pro Gly Gly Lys Thr Asp Glu
111 385 390 395 400
112 Pro Lys Gly Lys Thr Glu Ala Tyr Leu Glu Ala Ile Arg Lys Asn Ile
113 405 410 415
114 Glu Trp Leu Lys Lys His Asp Lys Lys Gly Asn Lys Glu Asp Tyr Asp
115 420 425 430
116 Leu Ser Lys Met Arg Asp Phe Ile Asn Lys Gln Ala Asp Ala Tyr Val
117 435 440 445
118 Glu Lys Gly Ile Leu Asp Lys Glu Glu Ala Glu Ala Ile Lys Arg Ile
119 450 455 460
120 Tyr Ser Ser Leu
121 465

```

123 (2) INFORMATION FOR SEQ ID NO: 2:

125 (i) SEQUENCE CHARACTERISTICS:

126 (A) LENGTH: 1844 base pairs

127 (B) TYPE: nucleic acid

128 (C) STRANDEDNESS: single

129 (D) TOPOLOGY: linear

131 (vii) IMMEDIATE SOURCE:

132 (A) LIBRARY: ISLTNOT01

133 (B) CLONE: 2379427

135 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

137 CAGCGCTCCC CTCTACCTGG AGACTTGACT CCCGCGCGCC CCAACCCTGC TTATCCCTTG 60
138 ACCGTCGAGT GTCAGAGATC CTGCAGCCGC CCAGTCCCGG CCCCTCTCCC GCCCCACACC 120
139 CACCCTCCTG GCTCTTCCTG TTTTACTCC TCCTTTTCAT TCATAACAAA AGCTACAGCT 180
140 CCAGGAGCCC AGCGCCGGGC TGTGACCCAA GCCGAGCGTG GAAGAATGGG GTTCCTCGGG 240
141 ACCGGCACTT GGATTCTGGT GTTAGTGCTC CCGATTCAAG CTTTCCCCAA ACCTGGAGGA 300
142 AGCCAAGACA AATCTCTACA TAATAGAGAA TTAAGTGCAG AAAGACCTTT GAATGAACAG 360
143 ATTGCTGAAG CAGAAGAAGA CAAGATTAAA AAAACATATC CTCCAGAAAA CAAGCCAGGT 420
144 CAGAGCAACT ATCTTTTGT TGATAACTTG AACCTGCTAA AGGCAATAAC AGAAAAGGAA 480
145 AAAATTGAGA AAGAAAGACA ATCTATAAGA AGCTCCCCAC TTGATAATAA GTTGAATGTG 540
146 GAAGATGTTG ATCAACCAA GAATCGAAAA CTGATCGATG ATTATGACTC TACTAAGAGT 600
147 GGATTGGATC ATAAATTTCA AGATGATCCA GATGGTCTTC ATCAACTAGA CGGGACTCCT 660
148 TTAACCGCTG AAGACATTGT CCATAAAATC GCTGCCAGGA TTTATGAAGA AAATGACAGA 720
149 GCCGTGTTTG ACAAGATTGT TTCTAACTA CTTAATCTCG GCCTTATCAC AGAAAGCCAA 780
150 GCACATACAC TGGAAGATGA AGTAGCAGAG GTTTTACAAA AATTAATCTC AAAGGAAGCC 840
151 AACAATTATG AGGAGGATCC CAATAAGCCC ACAAGCTGGA CTGAGAATCA GGCTGGAAAA 900
152 ATACCAGAGA AAGTGACTCC AATGGCAGCA ATTCAAGATG GTCTTGCTAA GGGAGAAAAAC 960
153 GATGAAACAG TATCTAACAC ATTAACCTTG ACAAATGGCT TGGAAAGGAG AACTAAAACC 1020
154 TACAGTGAAG ACAACTTTGA GGAACTCCAA TATTTCCTCA AATTCTATGC GCTACTGAAA 1080
155 AGTATTGATT CAGAAAAAGA AGCAAAAGAG AAAGAAACAC TGATTACTAT CATGAAAACA 1140
156 CTGATTGACT TTGTGAAGAT GATGGTGAAG TATGGAACAA TATCTCCAGA AGAAGGTGTT 1200
157 TCCTACCTTG AAAACTTGGA TGAAATGATT GCTCTTCAGA CCAAAAACAA GCTAGAAAAA 1260
158 AATGCTACTG ACAATATAAG CAAGCTTTTC CCAGCACCAT CAGAGAAGAG TCATGAAGAA 1320
159 ACAGACAGTA CCAAGGAAGA AGCAGCTAAG ATGGAAGGAG AATATGGAAG CTTGAAGGAT 1380
160 TCCACAAAAG ATGATAACTC CAACCCAGGA GGAAAGACAG ATGAACCCAA AGGAAAAACA 1440
161 GAAGCCTATT TGGAAGCCAT CAGAAAAAAT ATTGAATGGT TGAAGAAACA TGACAAAAAG 1500
162 GGAAATAAAG AAGATTATGA CCTTTCAAAG ATGAGAGACT TCATCAATAA ACAAGCTGAT 1560
163 GCTTATGTGG AGAAAGGCAT CCTTGACAAG GAAGAAGCCG AGGCCATCAA GCGCATTAT 1620

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164 AGCAGCCTGT AAAAATGGCA AAAGATCCAG GAGTCTTTCA ACTGTTTCAG AAAACATAAT 1680
165 ATAGCTTAAA ACACCTCTAA TTCTGTGATT AAAATTTTTT GACCCAAGGG TTATTAGAAA 1740
166 GTGCTGAATT TACAGTAGTT AACCTTTTAC AAGTGGTTAA AACATAGCTT TCTTCCCGTA 1800
167 AAAACTATCT GAAAGTAAAG TTGTATGTAA GCTGAAAAAA AAAA 1844

```

169 (2) INFORMATION FOR SEQ ID NO: 3:

171 (i) SEQUENCE CHARACTERISTICS:

172 (A) LENGTH: 153 amino acids

173 (B) TYPE: amino acid

174 (C) STRANDEDNESS: single

175 (D) TOPOLOGY: linear

177 (vii) IMMEDIATE SOURCE:

178 (A) LIBRARY: BRSTTUT14

179 (B) CLONE: 2744187

181 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

183 Met Ala Ala Gly Leu Phe Gly Leu Ser Ala Arg Arg Leu Leu Ala Ala
184 1 5 10 15
185 Ala Ala Thr Arg Gly Leu Pro Ala Ala Arg Val Arg Trp Glu Ser Ser
186 20 25 30
187 Phe Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala Gly Lys Arg Pro
188 35 40 45
189 Pro Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro Glu Pro Glu Asp Glu
190 50 55 60
191 Asn Leu Tyr Glu Lys Asn Pro Asp Ser His Gly Tyr Asp Lys Asp Pro
192 65 70 75 80
193 Val Leu Asp Val Trp Asn Met Arg Leu Val Phe Phe Phe Gly Val Ser
194 85 90 95
195 Ile Ile Leu Val Leu Gly Ser Thr Phe Val Ala Tyr Leu Pro Asp Tyr
196 100 105 110
197 Arg Met Lys Glu Trp Ser Arg Arg Glu Ala Glu Arg Leu Val Lys Tyr
198 115 120 125
199 Arg Glu Ala Asn Gly Leu Pro Ile Met Glu Ser Asn Cys Phe Asp Pro
200 130 135 140
201 Ser Lys Ile Gln Leu Pro Glu Asp Glu
202 145 150

```

204 (2) INFORMATION FOR SEQ ID NO: 4:

206 (i) SEQUENCE CHARACTERISTICS:

207 (A) LENGTH: 1463 base pairs

208 (B) TYPE: nucleic acid

209 (C) STRANDEDNESS: single

210 (D) TOPOLOGY: linear

212 (vii) IMMEDIATE SOURCE:

213 (A) LIBRARY: BRSTTUT14

214 (B) CLONE: 2744187

216 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

218 CAGCCGCTGG CTCCGTTTCA CTTCCCAGCC ACCCCCGCTG CTGCTACCAT GATCTGCCAG 60
219 CCTGGGTGAT GCTTCCTGCA GGGACTCTTC TCGGCCCGGG CTGTCAAGGA AGGGCTCCCA 120
220 GACATCACCT CTGCCCCGCC CCACCTCCTC CAACTCTCCC AGCTCAGCCG GAGCCGGAGC 180
221 GCGCAACAAC CAAGTCCGAG ACTGGAGGCA GATCGGGGGG AGGGGAGAAG CGCCAAGCGC 240
222 GCTGCCCTCC CAGGGAAACT CACTGCCGCC TACTCCAGC CGGCCACAGT CACCAGCTCA 300

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223 AAATGGCGAC GACGAGAAGG GAGTCGGCGC TCCGACCACC ATCCACCTAC TAAGGAAGCG 360
224 CGCTCTGGCC GGCCCCGGCG ATTGGTCACC GCGCGCTAGG GGACAGCCCT GGCCTCCTCT 420
225 GATTGGCAAG CGCTGGCCAC CTCCCCACAC CCCTTGCGAA CGCTCCCCTA GTGGAGAAAA 480
226 GGAGTAGCTA TTAGCCAATT CGGGCAGGGC CCGCTTTTGA GAAGCTTGAT TTCCTTTGAA 540
227 GATGAAAGAC TAGCGGAAGC TCTGCCTCTT TCCCCAGTGG GCGAGGGAAC TCGGGGCGAT 600
228 TGGCTGGGAA CTGTATCCAC CAAATGTCAC CGATTCTTCC TATGCAGGAA ATGAGCAGAC 660
229 CCATCAATAA GAAATTTCTC AGCCTGGCCG AAAATGGTTG GCGCCACGAA GCCACGACAA 720
230 CTGGAGGCAA AGAGGGTTGC TCAACGCCCC GCCTCATTGG AAAACCAAAT CAGATCTGGG 780
231 ACCTATATAG CTTGGCGGAG GCGGGGCGAT GATTGTCGCG CTCGCACCCA CTGCAGCTGC 840
232 GCACAGTCGC ATTTCTTTCC CCGCCCCCTGA GACCCTGCAG CACCATCTGT CATGGCGGCT 900
233 GGGCTGTTTG GTTTGAGCGC TCGCCGTCTT TTGGCGGCAG CGGCGACGCG AGGGCTCCCG 960
234 GCGGCCGCG TCCGCTGGGA ATCTAGCTTC TCCAGGACTG TGGTCGCCCC GTCCGCTGTG 1020
235 GCGGGAAAGC GGCCCCCAGA ACCGACCACA CCGTGGCAAG AGGACCCAGA ACCCGAGGAC 1080
236 GAAAACTTGT ATGAGAAGAA CCCAGACTCC CATGGTTATG ACAAGGACCC CGTTTTGGAC 1140
237 GTCTGGAACA TCGACTTGT CTTCTTCTTT GCGCTCTCCA TCATCCTGGT CCTTGGCAGC 1200
238 ACCTTTGTGG CCTATCTGCC TGACTACAGG ATGAAAGAGT GGTCCCGCCG CGAAGCTGAG 1260
239 AGGCTTGTGA AATACCGAGA GGCCAATGGC CTTCCTATCA TGGAATCCAA CTGCTTCGAC 1320
240 CCCAGCAAGA TCCAGCTGCC AGAGGATGAG TGACCAGTTG CTAAGTGGGG CTCAAGAAGC 1380
241 ACCGCCTTCC CCACCCCTG CCTGCCATTC TGACCTCTTC TCAGAGCACC TAATTAAAGG 1440
242 GGCTGAAAGT CTGAAAAAAA AAA 1463

```

244 (2) INFORMATION FOR SEQ ID NO: 5:

246 (i) SEQUENCE CHARACTERISTICS:

247 (A) LENGTH: 471 amino acids

248 (B) TYPE: amino acid

249 (C) STRANDEDNESS: single

250 (D) TOPOLOGY: linear

252 (vii) IMMEDIATE SOURCE:

253 (A) LIBRARY: GenBank

254 (B) CLONE: 413764

256 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```

258 Met Gly Phe Leu Trp Thr Gly Ser Trp Ile Leu Val Leu Val Leu Asn
259 1 5 10 15
260 Ser Gly Pro Ile Gln Ala Phe Pro Lys Pro Glu Gly Ser Gln Asp Lys
261 20 25 30
262 Ser Leu His Asn Arg Glu Leu Ser Ala Glu Arg Pro Leu Asn Glu Gln
263 35 40 45
264 Ile Ala Glu Ala Glu Ala Asp Lys Ile Lys Lys Ala Phe Pro Ser Glu
265 50 55 60
266 Ser Lys Pro Ser Glu Ser Asn Tyr Ser Ser Val Asp Asn Leu Asn Leu
267 65 70 75 80
268 Leu Arg Ala Ile Thr Glu Lys Glu Thr Val Glu Lys Glu Arg Gln Ser
269 85 90 95
270 Ile Arg Ser Pro Pro Phe Asp Asn Gln Leu Asn Val Glu Asp Ala Asp
271 100 105 110
272 Ser Thr Lys Asn Arg Lys Leu Ile Asp Glu Tyr Asp Ser Thr Lys Ser
273 115 120 125
274 Gly Leu Asp His Lys Phe Gln Asp Asp Pro Asp Gly Leu His Gln Leu
275 130 135 140
276 Asp Gly Thr Pro Leu Thr Ala Glu Asp Ile Val His Lys Ile Ala Thr

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## VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10077040.raw

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]